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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/985,911

DATE: 11/15/2001

TIME: 09:02:51

Input Set : A:\PF257D3-SeqList.txt

Output Set: N:\CRF3\11152001\I985911.raw

**ENTERED**

3 &lt;110&gt; APPLICANT: NI ET AL.

5 &lt;120&gt; TITLE OF INVENTION: HUMAN ENDOMETRIAL SPECIFIC STEROID-BINDING FACTOR I, II AND

III

7 &lt;130&gt; FILE REFERENCE: PF257D3

C--&gt; 9 &lt;140&gt; CURRENT APPLICATION NUMBER: US/09/985,911

10 &lt;141&gt; CURRENT FILING DATE: 2001-11-06

12 &lt;150&gt; PRIOR APPLICATION NUMBER: 09/583,169

13 &lt;151&gt; PRIOR FILING DATE: 2000-05-30

15 &lt;150&gt; PRIOR APPLICATION NUMBER: 09/263,810

16 &lt;151&gt; PRIOR FILING DATE: 1999-03-08

18 &lt;150&gt; PRIOR APPLICATION NUMBER: 08/821,451

19 &lt;151&gt; PRIOR FILING DATE: 1997-03-21

21 &lt;150&gt; PRIOR APPLICATION NUMBER: 60/014,724

22 &lt;151&gt; PRIOR FILING DATE: 1996-03-21

24 &lt;160&gt; NUMBER OF SEQ ID NOS: 27

26 &lt;170&gt; SOFTWARE: PatentIn version 3.1

28 &lt;210&gt; SEQ ID NO: 1

29 &lt;211&gt; LENGTH: 433

30 &lt;212&gt; TYPE: DNA

31 &lt;213&gt; ORGANISM: human

33 &lt;220&gt; FEATURE:

34 &lt;221&gt; NAME/KEY: CDS

35 &lt;222&gt; LOCATION: (43)..(312)

36 &lt;223&gt; OTHER INFORMATION:

39 &lt;220&gt; FEATURE:

40 &lt;221&gt; NAME/KEY: sig\_peptide

41 &lt;222&gt; LOCATION: (43)..(105)

42 &lt;223&gt; OTHER INFORMATION:

45 &lt;220&gt; FEATURE:

46 &lt;221&gt; NAME/KEY: mat\_peptide

47 &lt;222&gt; LOCATION: (106)..(312)

48 &lt;223&gt; OTHER INFORMATION:

51 &lt;400&gt; SEQUENCE: 1

52 tcactcattg tgaaagctga gctcacagcc gaataagcca cc atg agg ctg tca 54

53 Met Arg Leu Ser

54 -20

56 gtg tgt ctc ctg atg gtc tcg ctg gcc ctt tgc tgc tac cag gcc cat 102

57 Val Cys Leu Leu Met Val Ser Leu Ala Leu Cys Cys Tyr Gln Ala His

58 -15 -10 -5

60 gct ctt gtc tgc cca gct gtt gct tct gag atc aca gtc ttc tta ttc 150

61 Ala Leu Val Cys Pro Ala Val Ala Ser Glu Ile Thr Val Phe Leu Phe

62 -1 1 5 10 15

64 tta agt gac gct gcg gta aac ctc caa gtt gcc aaa ctt aat cca cct 198

65 Leu Ser Asp Ala Ala Val Asn Leu Gln Val Ala Lys Leu Asn Pro Pro

66 20 25 30

68 cca gaa gct ctt gca gcc aag ttg gaa gtg aag cac tgc acc gat cag 246

69 Pro Glu Ala Leu Ala Ala Lys Leu Glu Val Lys His Cys Thr Asp Gln

70 35 40 45

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72 ata tct ttt aag aaa cga ctc tca ttg gaa aaa gtc ctg gtg gaa ata      294
73 Ile Ser Phe Lys Lys Arg Leu Ser Leu Glu Lys Val Leu Val Glu Ile
74      50      55      60
76 gtg aaa aaa tgt ggt gtg tgacatgtaa aaatgctcaa cctgggtttcc      342
77 Val Lys Lys Cys Gly Val
78      65
80 aaagtctttc aacgacaccc tgatcttcaac taaaaattgt aaaggtttca acacgttgct      402
82 ttaataaaatc acttgccctg cacatcaaaa a      433
85 <210> SEQ ID NO: 2
86 <211> LENGTH: 90
87 <212> TYPE: PRT
88 <213> ORGANISM: human
90 <400> SEQUENCE: 2
92 Met Arg Leu Ser Val Cys Leu Leu Met Val Ser Leu Ala Leu Cys Cys
93      -20      -15      -10
96 Tyr Gln Ala His Ala Leu Val Cys Pro Ala Val Ala Ser Glu Ile Thr
97 -5      -1 1      5      10
100 Val Phe Leu Phe Leu Ser Asp Ala Ala Val Asn Leu Gln Val Ala Lys
101      15      20      25
104 Leu Asn Pro Pro Pro Glu Ala Leu Ala Ala Lys Leu Glu Val Lys His
105      30      35      40
108 Cys Thr Asp Gln Ile Ser Phe Lys Lys Arg Leu Ser Leu Glu Lys Val
109      45      50      55
112 Leu Val Glu Ile Val Lys Lys Cys Gly Val
113 60      65
116 <210> SEQ ID NO: 3
117 <211> LENGTH: 436
118 <212> TYPE: DNA
119 <213> ORGANISM: human
121 <220> FEATURE:
122 <221> NAME/KEY: CDS
123 <222> LOCATION: (40)..(309)
124 <223> OTHER INFORMATION:
127 <220> FEATURE:
128 <221> NAME/KEY: sig_peptide
129 <222> LOCATION: (40)..(102)
130 <223> OTHER INFORMATION:
133 <220> FEATURE:
134 <221> NAME/KEY: mat_peptide
135 <222> LOCATION: (103)..(309)
136 <223> OTHER INFORMATION:
139 <400> SEQUENCE: 3
140 ttgtttgtga aagctgagct cacagcaaaa caagccacc atg aag ctg tgc gtg      54
141      Met Lys Leu Ser Val
142      -20
144 tgt ctc ctg ctg gtc acg ctg gcc ctc tgc tgc tac cag gcc aat gcc      102
145 Cys Leu Leu Leu Val Thr Leu Ala Leu Cys Cys Tyr Gln Ala Asn Ala
146      -15      -10      -5      -1
148 gag ttc tgc cca gct ctt gtt tct gag ctg tta gac ttc ttc ttc att      150

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149 Glu Phe Cys Pro Ala Leu Val Ser Glu Leu Leu Asp Phe Phe Phe Ile
150 1          5          10          15
152 agt gaa cct ctg ttc aag tta agt ctt gcc aaa ttt gat gcc cct ccg      198
153 Ser Glu Pro Leu Phe Lys Leu Ser Leu Ala Lys Phe Asp Ala Pro Pro
154          20          25          30
156 gaa gct gtt gca gcc aag tta gga gtg aag aga tgc acg gat cag atg      246
157 Glu Ala Val Ala Ala Lys Leu Gly Val Lys Arg Cys Thr Asp Gln Met
158          35          40          45
160 tcc ctt cag aaa cga agc ctc att gcg gaa gtc ctg gtg aaa ata ttg      294
161 Ser Leu Gln Lys Arg Ser Leu Ile Ala Glu Val Leu Val Lys Ile Leu
162          50          55          60
164 aag aaa tgt agt gtg tgacatgtaa aaactttcat cctggtttcc actgtctttc      349
165 Lys Lys Cys Ser Val
166 65
168 aatgacaccc tgatcttcac tgcagaatgt aaaggtttca acgtcttgct ttaataaatc      409
170 acttgctctc caaaaaaaaa aaaaaaa      436
173 <210> SEQ ID NO: 4
174 <211> LENGTH: 90
175 <212> TYPE: PRT
176 <213> ORGANISM: human
178 <400> SEQUENCE: 4
180 Met Lys Leu Ser Val Cys Leu Leu Leu Val Thr Leu Ala Leu Cys Cys
181 -20          -15          -10
184 Tyr Gln Ala Asn Ala Glu Phe Cys Pro Ala Leu Val Ser Glu Leu Leu
185 -5          -1 1          5          10
188 Asp Phe Phe Phe Ile Ser Glu Pro Leu Phe Lys Leu Ser Leu Ala Lys
189          15          20          25
192 Phe Asp Ala Pro Pro Glu Ala Val Ala Ala Lys Leu Gly Val Lys Arg
193          30          35          40
196 Cys Thr Asp Gln Met Ser Leu Gln Lys Arg Ser Leu Ile Ala Glu Val
197          45          50          55
200 Leu Val Lys Ile Leu Lys Lys Cys Ser Val
201 60          65
204 <210> SEQ ID NO: 5
205 <211> LENGTH: 476
206 <212> TYPE: DNA
207 <213> ORGANISM: human
209 <220> FEATURE:
210 <221> NAME/KEY: CDS
211 <222> LOCATION: (46)..(330)
212 <223> OTHER INFORMATION:
215 <220> FEATURE:
216 <221> NAME/KEY: sig_peptide
217 <222> LOCATION: (46)..(108)
218 <223> OTHER INFORMATION:
221 <220> FEATURE:
222 <221> NAME/KEY: mat_peptide
223 <222> LOCATION: (109)..(330)
224 <223> OTHER INFORMATION:

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Input Set : A:\PF257D3-SeqList.txt

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227 <400> SEQUENCE: 5
228 acgagctgcc acgcacgact gaacacagac agcagccgcc tcgcc atg aag ctg ctg      57
229                                     Met Lys Leu Leu
230                                     -20
232 atg gtc ctc atg ctg gcg gcc ctc ctc ctg cac tgc tat gca gat tct      105
233 Met Val Leu Met Leu Ala Ala Leu Leu Leu His Cys Tyr Ala Asp Ser
234 -15 -10 -5
236 ggc tgc aaa ctc ctg gag gac atg gtt gaa aag acc atc aat tcc gac      153
237 Gly Cys Lys Leu Leu Glu Asp Met Val Glu Lys Thr Ile Asn Ser Asp
238 -1 1 5 10 15
240 ata tct ata cct gaa tac aaa gag ctt ctt caa gag ttc ata gac agt      201
241 Ile Ser Ile Pro Glu Tyr Lys Glu Leu Leu Gln Glu Phe Ile Asp Ser
242 20 25 30
244 gat gcc gct gca gag gct atg ggg aaa ttc aag cag tgt ttc ctc aac      249
245 Asp Ala Ala Ala Glu Ala Met Gly Lys Phe Lys Gln Cys Phe Leu Asn
246 35 40 45
248 cag tca cat aga act ctg aaa aac ttt gga ctg atg atg cat aca gtg      297
249 Gln Ser His Arg Thr Leu Lys Asn Phe Gly Leu Met Met His Thr Val
250 50 55 60
252 tac gac agc att tgg tgt aat atg aag agt aat taactttacc caaggcgttt      350
253 Tyr Asp Ser Ile Trp Cys Asn Met Lys Ser Asn
254 65 70
256 ggctcagagg gctacagact atggccagaa ctcatctgtt gattgctaga aaccactttc      410
258 ttcttgtgtt gctttttatg tgggaactgc tagacaactg ttgaaacctc aattcattcc      470
260 atttca      476
263 <210> SEQ ID NO: 6
264 <211> LENGTH: 95
265 <212> TYPE: PRT
266 <213> ORGANISM: human
268 <400> SEQUENCE: 6
270 Met Lys Leu Leu Met Val Leu Met Leu Ala Ala Leu Leu Leu His Cys
271 -20 -15 -10
274 Tyr Ala Asp Ser Gly Cys Lys Leu Leu Glu Asp Met Val Glu Lys Thr
275 -5 -1 1 5 10
278 Ile Asn Ser Asp Ile Ser Ile Pro Glu Tyr Lys Glu Leu Leu Gln Glu
279 15 20 25
282 Phe Ile Asp Ser Asp Ala Ala Ala Glu Ala Met Gly Lys Phe Lys Gln
283 30 35 40
286 Cys Phe Leu Asn Gln Ser His Arg Thr Leu Lys Asn Phe Gly Leu Met
287 45 50 55
290 Met His Thr Val Tyr Asp Ser Ile Trp Cys Asn Met Lys Ser Asn
291 60 65 70
294 <210> SEQ ID NO: 7
295 <211> LENGTH: 24
296 <212> TYPE: DNA
297 <213> ORGANISM: Artificial Sequence
299 <220> FEATURE:
300 <221> NAME/KEY: Primer_Bind
301 <223> OTHER INFORMATION: Synthetic oligonucleotide

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Input Set : A:\PF257D3-SeqList.txt

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303 <400> SEQUENCE: 7
304 cgcgcgatgct tgtctgccca gctg 24
307 <210> SEQ ID NO: 8
308 <211> LENGTH: 24
309 <212> TYPE: DNA
310 <213> ORGANISM: Artificial Sequence
312 <220> FEATURE:
313 <221> NAME/KEY: Primer_Bind
314 <223> OTHER INFORMATION: Synthetic oligonucleotide
316 <400> SEQUENCE: 8
317 cgcccatgga gttctgccca gctc 24
320 <210> SEQ ID NO: 9
321 <211> LENGTH: 24
322 <212> TYPE: DNA
323 <213> ORGANISM: Artificial Sequence
325 <220> FEATURE:
326 <221> NAME/KEY: Primer_Bind
327 <223> OTHER INFORMATION: Synthetic oligonucleotide
329 <400> SEQUENCE: 9
330 cgcgcgatgca ctgctatgca gatt 24
333 <210> SEQ ID NO: 10
334 <211> LENGTH: 24
335 <212> TYPE: DNA
336 <213> ORGANISM: Artificial Sequence
338 <220> FEATURE:
339 <221> NAME/KEY: Primer_Bind
340 <223> OTHER INFORMATION: Synthetic oligonucleotide
342 <400> SEQUENCE: 10
343 cgcaagcttc atttttacat gtca 24
346 <210> SEQ ID NO: 11
347 <211> LENGTH: 24
348 <212> TYPE: DNA
349 <213> ORGANISM: Artificial Sequence
351 <220> FEATURE:
352 <221> NAME/KEY: Primer_Bind
353 <223> OTHER INFORMATION: Synthetic oligonucleotide
355 <400> SEQUENCE: 11
356 cgcaagctta gtttttacat gtca 24
359 <210> SEQ ID NO: 12
360 <211> LENGTH: 27
361 <212> TYPE: DNA
362 <213> ORGANISM: Artificial Sequence
364 <220> FEATURE:
365 <221> NAME/KEY: Primer_Bind
366 <223> OTHER INFORMATION: Synthetic oligonucleotide
368 <400> SEQUENCE: 12
369 cgcaagctta cgccttggtt aaagtta 27
372 <210> SEQ ID NO: 13
373 <211> LENGTH: 35

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/985,911

DATE: 11/15/2001

TIME: 09:02:52

Input Set : A:\PF257D3-SeqList.txt

Output Set: N:\CRF3\11152001\I985911.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application Number